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RAW SEQUENCE LISTING

DATE: 04/25/2002

PATENT APPLICATION: US/09/989,903

TIME: 14:54:29

Input Set : A:\434dl.app

Output Set: N:\CRF3\04252002\I989903.raw

p6

3 <110> APPLICANT: Alnemri, Emad S.
 4 Fernandez-Alnemri, Teresa
 7 <120> TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
 8 AND METHODS OF USE
 10 <130> FILE REFERENCE: 480140.434D1
 12 <140> CURRENT APPLICATION NUMBER: US 09/989,903
 C--> 13 <141> CURRENT FILING DATE: 2002-04-11
 15 <160> NUMBER OF SEQ ID NOS: 78
 17 <170> SOFTWARE: PatentIn Ver. 2.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 850
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Mus musculus
 24 <220> FEATURE:
 25 <221> NAME/KEY: modified_base
 26 <222> LOCATION: (537)
 27 <223> OTHER INFORMATION: Where n is Adenine, Cytosine, Guanine or Thymine
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 31 atggagtcag agatgagtga tcctcagcca ttgcaggagg aaagatatga tatgtcaggt 120
 32 gcccgctgg ccttgacgct gtgtgtcacc aaagcccggg agggttccga ggtagacatg 180
 33 gaggccctgg aacgcattgt cggttacctg aaatttgaaa gcaccatgaa gagggatccc 240
 34 accgcccagc aattttctgga agagttggat gaatttcagc agaccataga taattgggaa 300
 35 gagcctgtca gctgtgctt tgtgtactc atggcacatg gtgaggaagg cctcctcaag 360
 36 ggagaagatg agaagatggt cagactagaa gaccttttg aagtcttgaa caacaagaac 420
 37 tgcaaggccc tgagaggcaa gccaaagggtg tacatcatcc aggctttag aggagagcac 480
 X-> 38 agagaccccg gtgaggaact acgtggaaat gaggaactag gtggagatga ggaactnggt 540
 39 ggagatgagg ttgctgtgct caagaacaac ccccaaagta tcccaaccta tacggatacc 600
 40 ctccacatct actccacggt agaggggtac ctctcctata gacatgacga gaaaggctct 660
 41 ggcttcatcc agaccctgac ggatgtgttc attcataaaa aaggatccat cttagaactg 720
 42 acagaagaga tcaccgcact tatggcaaac acggagggtga tgcaggaagg aaaaccaagg 780
 43 aaagtgaacc ctgaagtcca aagcaccctc cggaagaagc tctatttgca ataaaagaga 840
 44 gggcagggat 850
 46 <210> SEQ ID NO: 2
 47 <211> LENGTH: 260
 48 <212> TYPE: PRT
 49 <213> ORGANISM: Mus musculus
 51 <400> SEQUENCE: 2
 52 Lys Pro Asp Met Glu Ser Glu Met Ser Asp Pro Gln Pro Leu Gln Glu
 53 -3 -1 1 5 10
 55 Glu Arg Tyr Asp Met Ser Gly Ala Arg Leu Ala Leu Thr Leu Cys Val
 56 15 20 25
 58 Thr Lys Ala Arg Glu Gly Ser Glu Val Asp Met Glu Ala Leu Glu Arg

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Input Set : A:\434d1.app

Output Set: N:\CRF3\04252002\I989903.raw

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59 30          35          40          45
61 Met Phe Arg Tyr Leu Lys Phe Glu Ser Thr Met Lys Arg Asp Pro Thr
62          50          55          60
64 Ala Gln Gln Phe Leu Glu Glu Leu Asp Glu Phe Gln Gln Thr Ile Asp
65          65          70          75
67 Asn Trp Glu Glu Pro Val Ser Cys Ala Phe Val Val Leu Met Ala His
68          80          85          90
70 Gly Glu Glu Gly Leu Leu Lys Gly Glu Asp Glu Lys Met Val Arg Leu
71          95          100          105
73 Glu Asp Leu Phe Glu Val Leu Asn Asn Lys Asn Cys Lys Ala Leu Arg
74 110          115          120          125
76 Gly Lys Pro Lys Val Tyr Ile Ile Gln Ala Cys Arg Gly Glu His Arg
77          130          135          140
79 Asp Pro Gly Glu Glu Leu Arg Gly Asn Glu Glu Leu Gly Gly Asp Glu
80          145          150          155
82 Glu Leu Gly Gly Asp Glu Val Ala Val Leu Lys Asn Asn Pro Gln Ser
83          160          165          170
85 Ile Pro Thr Tyr Thr Asp Thr Leu His Ile Tyr Ser Thr Val Glu Gly
86          175          180          185
88 Tyr Leu Ser Tyr Arg His Asp Glu Lys Gly Ser Gly Phe Ile Gln Thr
89 190          195          200          205
91 Leu Thr Asp Val Phe Ile His Lys Lys Gly Ser Ile Leu Glu Leu Thr
92          210          215          220
94 Glu Glu Ile Thr Arg Leu Met Ala Asn Thr Glu Val Met Gln Glu Gly
95          225          230          235
97 Lys Pro Arg Lys Val Asn Pro Glu Val Gln Ser Thr Leu Arg Lys Lys
98          240          245          250
100 Leu Tyr Leu Gln
101          255
103 <210> SEQ ID NO: 3
104 <211> LENGTH: 5
105 <212> TYPE: PRT
106 <213> ORGANISM: Mus musculus
108 <400> SEQUENCE: 3
109 Gln Ala Cys Arg Gly
110 1 5
113 <210> SEQ ID NO: 4
114 <211> LENGTH: 777
115 <212> TYPE: DNA
116 <213> ORGANISM: Homo sapien
118 <220> FEATURE:
119 <221> NAME/KEY: CDS
120 <222> LOCATION: (49)...(774)
122 <400> SEQUENCE: 4
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124 Met Ser Asn
125 1
127 ccg cgg tct ttg gaa gag gag aaa tat gat atg tca ggt gcc gcg ctg 105
128 Pro Arg Ser Leu Glu Glu Glu Lys Tyr Asp Met Ser Gly Ala Ala Leu

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129      5      10      15
131 gcc cta ata ctg tgt gtc acc aaa gcc cgg gaa ggt tcc gaa gaa gac 153
132 Ala Leu Ile Leu Cys Val Thr Lys Ala Arg Glu Gly Ser Glu Glu Asp
133 20      25      30      35
135 ctg gat gct ctg gaa cac atg ttt cgg cag ctg aga ttc gaa agc acc 201
136 Leu Asp Ala Leu Glu His Met Phe Arg Gln Leu Arg Phe Glu Ser Thr
137      40      45      50
139 atg aaa aga gac ccc act gcc gag caa ttc cag gaa gag ctg gaa aaa 249
140 Met Lys Arg Asp Pro Thr Ala Glu Gln Phe Gln Glu Glu Leu Glu Lys
141      55      60      65
143 ttc cag cag gcc atc gat tcc cgg gaa gat ccc gtc agt tgt gcc ttc 297
144 Phe Gln Gln Ala Ile Asp Ser Arg Glu Asp Pro Val Ser Cys Ala Phe
145      70      75      80
147 gtg gta ctc atg gct cac ggg agg gaa ggc ttc ctc aag gga gaa gat 345
148 Val Val Leu Met Ala His Gly Arg Glu Gly Phe Leu Lys Gly Glu Asp
149      85      90      95
151 ggg gag atg gtc aag ctg gag aat ctc ttc gag gcc ctg aac aac aag 393
152 Gly Glu Met Val Lys Leu Glu Asn Leu Phe Glu Ala Leu Asn Asn Lys
153 100      105      110      115
155 aac tgc cag gcc ctg cga gct aag ccc aag gtg tac atc ata cag gcc 441
156 Asn Cys Gln Ala Leu Arg Ala Lys Pro Lys Val Tyr Ile Ile Gln Ala
157      120      125      130
159 tgt cga gga gaa caa agg gac ccc ggt gaa aca gta ggt gga gat gag 489
160 Cys Arg Gly Glu Gln Arg Asp Pro Gly Glu Thr Val Gly Gly Asp Glu
161      135      140      145
163 att gtg atg gtc atc aaa gac agc cca caa acc atc cca aca tac aca 537
164 Ile Val Met Val Ile Lys Asp Ser Pro Gln Thr Ile Pro Thr Tyr Thr
165      150      155      160
167 gat gcc ttg cac gtt tat tcc acg gta gag gga tac atc gcc tac cga 585
168 Asp Ala Leu His Val Tyr Ser Thr Val Glu Gly Tyr Ile Ala Tyr Arg
169      165      170      175
171 cat gat cag aaa ggc tca tgc ttt atc cag acc ctg gtg gat gtg ttc 633
172 His Asp Gln Lys Gly Ser Cys Phe Ile Gln Thr Leu Val Asp Val Phe
173 180      185      190      195
175 acg aag agg aaa gga cat atc ttg gaa ctt ctg aca gag gtg acc cgg 681
176 Thr Lys Arg Lys Gly His Ile Leu Glu Leu Leu Thr Glu Val Thr Arg
177      200      205      210
179 cgg atg gca gaa gca gag ctg gtt caa gaa gga aaa gca agg aaa acg 729
180 Arg Met Ala Glu Ala Glu Leu Val Gln Glu Gly Lys Ala Arg Lys Thr
181      215      220      225
183 aac cct gaa atc caa agc acc ctc cgg aaa cgg ctg tat ctg cag 774
184 Asn Pro Glu Ile Gln Ser Thr Leu Arg Lys Arg Leu Tyr Leu Gln
185      230      235      240
187 tag 777
189 <210> SEQ ID NO: 5
190 <211> LENGTH: 242
191 <212> TYPE: PRT
192 <213> ORGANISM: Homo sapien
194 <400> SEQUENCE: 5

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195 Met Ser Asn Pro Arg Ser Leu Glu Glu Glu Lys Tyr Asp Met Ser Gly
196 1 5 10 15
197 Ala Ala Leu Ala Leu Ile Leu Cys Val Thr Lys Ala Arg Glu Gly Ser
198 20 25 30
199 Glu Glu Asp Leu Asp Ala Leu Glu His Met Phe Arg Gln Leu Arg Phe
200 35 40 45
201 Glu Ser Thr Met Lys Arg Asp Pro Thr Ala Glu Gln Phe Gln Glu Glu
202 50 55 60
203 Leu Glu Lys Phe Gln Gln Ala Ile Asp Ser Arg Glu Asp Pro Val Ser
204 65 70 75 80
205 Cys Ala Phe Val Val Leu Met Ala His Gly Arg Glu Gly Phe Leu Lys
206 85 90 95
207 Gly Glu Asp Gly Glu Met Val Lys Leu Glu Asn Leu Phe Glu Ala Leu
208 100 105 110
209 Asn Asn Lys Asn Cys Gln Ala Leu Arg Ala Lys Pro Lys Val Tyr Ile
210 115 120 125
211 Ile Gln Ala Cys Arg Gly Glu Gln Arg Asp Pro Gly Glu Thr Val Gly
212 130 135 140
213 Gly Asp Glu Ile Val Met Val Ile Lys Asp Ser Pro Gln Thr Ile Pro
214 145 150 155 160
215 Thr Tyr Thr Asp Ala Leu His Val Tyr Ser Thr Val Glu Gly Tyr Ile
216 165 170 175
217 Ala Tyr Arg His Asp Gln Lys Gly Ser Cys Phe Ile Gln Thr Leu Val
218 180 185 190
219 Asp Val Phe Thr Lys Arg Lys Gly His Ile Leu Glu Leu Leu Thr Glu
220 195 200 205
221 Val Thr Arg Arg Met Ala Glu Ala Glu Leu Val Gln Glu Gly Lys Ala
222 210 215 220
223 Arg Lys Thr Asn Pro Glu Ile Gln Ser Thr Leu Arg Lys Arg Leu Tyr
224 225 230 235 240
225 Leu Gln
228 <210> SEQ ID NO: 6
229 <211> LENGTH: 850
230 <212> TYPE: DNA
231 <213> ORGANISM: Homo sapien
233 <220> FEATURE:
234 <221> NAME/KEY: CDS
235 <222> LOCATION: (48)...(737)
237 <400> SEQUENCE: 6
238 aggatcagac aagggtgctg agagccggac tcacaaccaa aggagaa atg agc aat 56
239 Met Ser Asn
240 1
242 ccg cgg tct ttg gaa gag gag aaa tat gat atg tca ggt gcc cgc ctg 104
243 Pro Arg Ser Leu Glu Glu Lys Tyr Asp Met Ser Gly Ala Arg Leu
244 5 10 15
246 gcc cta ata ctg tgt gtc acc aaa gcc cgg gaa ggt tcc gaa gaa gac 152
247 Ala Leu Ile Leu Cys Val Thr Lys Ala Arg Glu Gly Ser Glu Glu Asp
248 20 25 30 35
250 ctg gat gct ctg gaa cac atg ttt cgg cag ctg aga ttc gaa agc acc 200

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Input Set : A:\434dl.app

Output Set: N:\CRF3\04252002\I989903.raw

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251 Leu Asp Ala Leu Glu His Met Phe Arg Gln Leu Arg Phe Glu Ser Thr
252          40          45          50
254 atg aaa aga gac ccc act gcc gag caa ttc cag gaa gag ctg gaa aaa      248
255 Met Lys Arg Asp Pro Thr Ala Glu Gln Phe Gln Glu Glu Leu Glu Lys
256          55          60          65
258 ttc cag cag gcc atc gat tcc cgg gaa gat ccc gtc agt tgt gcc ttc      296
259 Phe Gln Gln Ala Ile Asp Ser Arg Glu Asp Pro Val Ser Cys Ala Phe
260          70          75          80
262 gtg gta ctc atg gct cac ggg agg gaa ggc ttc ctc aag gga gaa gat      344
263 Val Val Leu Met Ala His Gly Arg Glu Gly Phe Leu Lys Gly Glu Asp
264          85          90          95
266 ggg gag atg gtc aag ctg gag aat ctc ttc gag gcc ctg aac aac aag      392
267 Gly Glu Met Val Lys Leu Glu Asn Leu Phe Glu Ala Leu Asn Asn Lys
268 100          105          110          115
270 aac tgc cag gcc ctg cga gct aag ccc aag gtg tac atc ata cag gcc      440
271 Asn Cys Gln Ala Leu Arg Ala Lys Pro Lys Val Tyr Ile Ile Gln Ala
272          120          125          130
274 tgt cga gga gaa caa agg gac ccc ggt gaa aca gta ggt gga gat gag      488
275 Cys Arg Gly Glu Gln Arg Asp Pro Gly Glu Thr Val Gly Gly Asp Glu
276          135          140          145
278 att gtg atg gtc atc aaa gac agc cca caa acc atc cca aca tac aca      536
279 Ile Val Met Val Ile Lys Asp Ser Pro Gln Thr Ile Pro Thr Tyr Thr
280          150          155          160
282 gat gcc ttg cac gtt tat tcc acg gta gag gga ccc acg ccc ttc cag      584
283 Asp Ala Leu His Val Tyr Ser Thr Val Glu Gly Pro Thr Pro Phe Gln
284          165          170          175
286 gat ccc ctc tac cta ccc tct gaa gct ccc ccg aac cca cct ctc tgg      632
287 Asp Pro Leu Tyr Leu Pro Ser Glu Ala Pro Pro Asn Pro Pro Leu Trp
288 180          185          190          195
290 aat tcc cag gat aca tcg cct acc gac atg atc aga aag gct cat gct      680
291 Asn Ser Gln Asp Thr Ser Pro Thr Asp Met Ile Arg Lys Ala His Ala
292          200          205          210
294 tta tcc aga ccc tgg tgg atg tgt tca cga aga gga aag gac ata tct      728
295 Leu Ser Arg Pro Trp Trp Met Cys Ser Arg Arg Gly Lys Asp Ile Ser
296          215          220          225
298 tgg aac ttc tgacagaggt gacccggcgg atggcagaag cagagctggt      777
299 Trp Asn Phe
300          230
302 tcaagaagga aaagcaagga aaacgaaccc tgaaatccaa agcaccctcc ggaaacggct      837
303 gtatctgcag tag      850
305 <210> SEQ ID NO: 7
306 <211> LENGTH: 230
307 <212> TYPE: PRT
308 <213> ORGANISM: Homo sapien
310 <400> SEQUENCE: 7
311 Met Ser Asn Pro Arg Ser Leu Glu Glu Glu Lys Tyr Asp Met Ser Gly
312 1          5          10          15
313 Ala Arg Leu Ala Leu Ile Leu Cys Val Thr Lys Ala Arg Glu Gly Ser
314          20          25          30

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RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\434dl.app
Output Set: N:\CRF3\04252002\I989903.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 537
Seq#:76; N Pos. 537